SEQUENCE LISTING

Vander Horn, Peter B. MJ Bioworks, Inc. <120> Methods of Making Hybrid Proteins <130> 020130-001420US <140> US 10/627,592 <141> 2003-07-25 <150> US 60/463,781 <151> 2003-04-17 <150> US 60/483,287 <151> 2003-06-27 <160> 50 <170> PatentIn Ver. 2.1 <210> 1 <211> 493 <212> PRT <213> Artificial Sequence <220>

<223> Description of Artificial Sequence:BlastP alignment Pyrococcus furiosus DNA polymerase (Pfu) query sequence

<400> 1 Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg 2.0

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg 50

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 125

Met Glu Gly Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr 130 135

Leu 145	Tyr	His	Glu	Gly	Glu 150	Glu	Phe	Gly	Lys	Gly 155	Pro	Ile	Ile	Met	Ile 160
Ser	Tyr	Ala	Asp	Glu 165	Asn	Glu	Ala	Lys	Val 170	Ile	Thr	Trp	Lys	Asn 175	Ile
Asp	Leu	Pro	Tyr 180	Val	Glu	Val	Val	Ser 185	Ser	Glu	Arg	Glu	Met 190	Ile	Lys
Arg	Phe	Leu 195	Arg	Ile	Ile	Arg	Glu 200	Lys	Asp	Pro	Asp	Ile 205	Ile	Val	Thr
Tyr	Asn 210	Gly	Asp	Ser	Phe	Asp 215	Phe	Pro	Tyr	Leu	Ala 220	Lys	Arg	Ala	Glu
Lys 225	Leu	Gly	Ile	Lys	Leu 230	Thr	Ile	Gly	Arg	Asp 235	Gly	Ser	Glu	Pro	Lys 240
Met	Gln	Arg	Ile	Gly 245	Asp	Met	Thr	Ala	Val 250	Glu	Val	Lys	Gly	Arg 255	Ile
His	Phe	Asp _.	Leu 260	Tyr	His	Val	Ile	Thr 265	Arg	Thr	Ile	Asn	Leu 270	Pro	Thr
Tyr	Thr	Leu 275	Glu	Ala	Val	Tyr	Glu 280	Ala	Ile	Phe	Gly	Lys 285	Pro	Lys	Glu
Lys	Val 290	Tyr	Ala	Asp	Glu	Ile 295	Ala	Lys	Ala	Trp	Glu 300	Ser	Gly	Glu	Asn
Leu 305	Glu	Arg	Val	Ala	Lys 310	Tyr	Ser	Met	Glu	Asp 315	Ala	Lys	Ala	Thr	Tyr 320
Glu	Leu	Gly	Lys	Glu 325	Phe	Leu	Pro	Met	Glu 330	Ile	Gln	Leu	Ser	Arg 335	Leu
Val	Gly	Gln	Pro 340	Leu	Trp	Asp	Val	Ser 345	Arg	Ser	Ser	Thr	Gly 350	Asn	Leu
Val	Glu	Trp 355	Phe	Leu	Leu	Arg	Lys 360	Ala	Tyr	Glu	Arg	Asn 365	Glu	Val	Ala
Pro	Asn 370	Lys	Pro	Ser	Glu	Glu 375	Glu	Týr	Gln	Arg	Arg 380	Leu	Arg	Glu	Ser
Tyr 385	Thr	Gly	Gly	Phe	Val 390	Lys	Glu	Pro	Glu	Lys 395	Gly	Leu	Trp	Glu	Asn 400
Ile	Val	Tyr	Leu	Asp 405	Phe	Arg	Ala	Leu	Tyr 410	Pro	Ser	Ile	Ile	Ile 415	Thr
His	Asn	Val	Ser 420	Pro	Asp	Thr	Leu	Asn 425	Leu	Glu	Gly	Cys	Lys 430	Asn	Tyr
Asp	Ile	Ala 435	Pro	Gln	Val	Gly	His 440	Lys	Phe	Сув	Lys	Asp 445	Ile	Pro	Gly
Phe	Ile 450	Pro	Ser	Leu	Leu	Gly 455	His	Leu	Leu	Glu	Glu 460	Arg	Gln	Lys	Ile

Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu 465 470 475 480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser 485 490

<210> 2

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:BlastP
 alignment Pyrococcus furiosus DNA polymerase (Pfu)
 query sequence

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Asn Ser Phe Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys

1 10 15

Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu 20 25 30

Leu Val Trp Lys Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr
35 40 45

Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu 50 55 60

Glu Ile Lys Lys Lys Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys 65 70 75 80

Leu Pro Gly Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly
85 90 95

Phe Phe Val Thr Lys Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys 100 105 110

Val Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile 115 120 125

Ala Lys Glu Thr Gln Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly 130 135 140

Asp Val Glu Glu Ala Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu 145 150 155 160

Ala Asn Tyr Glu Ile Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile 165 170 175

Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val 180 185 190

Ala Lys Lys Leu Ala Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val 195 200 205

Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala 210 215 220 Ile Leu Ala Glu Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu 225 230 235 240

Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu 245 250 255

Gly Phe Gly Tyr Arg Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln 260 265 270

Val Gly Leu Thr Ser Trp Leu Asn Ile Lys Lys 275 280

<210> 3

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:BlastP
 alignment Pyrococcus sp. GB-D DNA polymerase (Deep
 Vent) subject sequence

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Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile 1 5 10 15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg 20 25 30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Gln Ile 35 40 45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg 50 55 60

Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile 65 70 75 80

Glu Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile 85 90 95

Arg Asp Lys Ile Arg Glu His Ser Ala Val Ile Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro

Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

<210> 4

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:BlastP
 alignment Pyrococcus sp. GB-D DNA polymerase (Deep
 Vent) subject sequence

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Asn Ser Tyr Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys

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Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu 20 25 30

Phe Val Arg Lys Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr 35 40 45

Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Ala Lys Pro Glu
50 60

Glu Ile Lys Lys Lys Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys 65 70 75 80

Leu Pro Gly Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly
85 90 95

Phe Phe Val Thr Lys Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys
100 105 110

Ile Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile
115 120 125 .

Ala Lys Glu Thr Gln Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly 130 135 140

Asn Val Glu Glu Ala Val Lys Ile Val Lys Glu Val Thr Glu Lys Leu 145 150 155 160

Ser Lys Tyr Glu Ile Pro Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile 165 170 175

Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val 180 185 190

Ala Lys Arg Leu Ala Ala Arg Gly Val Lys Val Arg Pro Gly Met Val 195 200 205

Ile Glý Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala 210 215 220

Ile Leu Ala Glu Glu Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu 225 230 235 240

Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu 245 250 255 Ala Phe Gly Tyr Arg Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln 260 265 270

Thr Gly Leu Thr Ala Trp Leu Asn Ile Lys Lys 275 280

<21.0> 5

<211> 493

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:BlastP
 alignment consensus sequence

<220>

<221> MOD RES

<222> (1)..(493)

<223> Xaa = unknown amino acid

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Arg Xaa Phe Lys Lys Glu Asn Gly Xaa Phe Lys Xaa Glu Xaa Asp Arg
20 25 30

Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile 35 40 45

Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg 50 55 60

Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile 65 70 75 80

Xaa Val Trp Xaa Leu Tyr Xaa Glu His Pro Gln Asp Val Pro Xaa Ile 85 90 95

Arg Xaa Lys Xaa Arg Glu His Xaa Ala Val Xaa Asp Ile Phe Glu Tyr 100 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Gly Xaa Glu Glu Leu Lys Xaa Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Xaa Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Xaa Glu Ala Lys Val Ile Thr Trp Lys Xaa Ile 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

Arg Phe Leu Xaa Xaa Ile Arg Glu Lys Asp Pro Asp Xaa Ile Xaa Thr 195 200 205

Tyr	Asn 210	Gly	Asp	Ser	Phe	Asp 215	Xaa	Pro	Tyr	Leu	Xaa 220	Lys	Arg	Ala	Glu
Lys 225	Leu	Gly	Ile	Lys	Leu 230	Xaa	Xaa	Gly	Arg	Asp 235	Gly	Ser	Glu	Pro	Lys 240
Met	Gln	Arg	Xaa	Gly 245	Asp	Met	Thr	Ala	Val 250	Glu	Xaa	Lys	Gly	Arg 255	Ile
His	Phe	Asp	Leu 260	Tyr	His	Val	Ile	Xaa 265	Arg	Thr	Ile	Asn	Leu 270	Pro	Thr
Tyr	Thr	Leu 275	Glu	Ala	Val	Tyr	Glu 280	Ala	Ile	Phe	Gly	Lys 285	Pro	Lys	Glu
Lys	Val 290	Tyr	Ala	Xaa	Glu	Ile 295	Ala	Xaa	Ala	Trp	Glu 300	Xaa	Gly	Xaa	Xaa
Leu 305	Glu	Arg	Val	Ala	Lys 310	Tyr	Ser	Met	Glu	Asp 315	Ala	Lys	Xaa	Thr	Tyr 320
Glu	Leu	Gly	Xaa	Glu 325	Phe	Xaa	Pro _.	Met	Glu 330	Xaa	Gln	Leu	Ser	Arg 335	Leu
Val	Gly	Gln	Pro 340	Leu	Trp	Asp	Val	Ser 345	Arg	Ser	Ser	Thr	Gly 350	Asn	Leu
Val	Glu	Trp 355	Xaa	Leu	Leu	Arg	Lys 360	Ala	Tyr	Glu	Arg	Asn 365	Glu	Xaa	Ala
Pro	Asn 370	Lys	Pro	Xaa	Glu	Xaa 375	Glu	Tyr	Xaa	Arg	Arg 380	Leu	Arg	Glu	Ser
Tyr 385	Xaa	Gly	Gly	Xaa	Val 390	Lys	Glu	Pro	Glu	Lys 395	Gly	Leu	Trp	Glu	Xaa 400
Xaa	Val	Xaa	Leu	Asp 405	Phe	Arg	Xaa	Leu	Tyr 410	Pro	Ser	Ile	Ile	Ile 415	Thr
His	Asn	Val	Ser 420	Pro	Asp	Thr	Leu	Asn 425	Xaa	Glu	Gly	Cys	Xaa 430	Xaa	Tyr
Asp	Xaa	Ala 435	Pro	Xaa	Val	Gly	His 440	Lys	Phe	Cys	Lys	Asp 445	Xaa	Pro	Gly
Phe	Ile 450	Pro	Ser	Leu	Leu	Xaa 455	Xaa	Leu	Leu	Xaa	Glu 460	Arg	Gln	Xaa	Ile
Lys 465	Xaa	Lys	Met	Lys	Xaa 470	Xaa	Xaa	Asp	Pro	Ile 475	Glu	Lys	Xaa	Xaa	Leu 480
Asp	Tyr	Arg	Gln	Xaa 485	Ala	Ile	Lys	Xaa	Leu 490	Ala	Asn	Ser			

<210> 6

<211> 283

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:BlastP alignment consensus sequence

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<221> MOD RES

<222> (1)..(283)

<223> Xaa = unknown amino acid

<400> 6

Asn Ser Xaa Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys
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Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu 20 25 30

Xaa Val Xaa Lys Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr 35 40 45

Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Xaa Xaa Xaa Glu 50 60

Glu Ile Lys Lys Lys Ala Leu Glu Phe Val Xaa Tyr Ile Asn Xaa Lys 65 70 75 80

Leu Pro Gly Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly 85 90 95

Phe Phe Val Thr Lys Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys 100 105 110

Xaa Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile 115 120 125

Ala Lys Glu Thr Gln Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly 130 135 140

Xaa Xaa Tyr Glu Ile Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile 165 170 175

Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val

Ala Lys Xaa Leu Ala Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val 195 200 205

Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala 210 215 220

Ile Leu Ala Glu Glu Xaa Asp Xaa Xaa Lys His Lys Tyr Asp Ala Glu 225 230 235 240

Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu 245 250 255 Xaa Phe Gly Tyr Arg Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln 265 Xaa Gly Leu Thr Xaa Trp Leu Asn Ile Lys Lys 280 <210> 7 <211> 151 <212> PRT <213> Escherichia coli <220> <223> mesophile E. coli deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase or Dut) (ECD) <400> 7 Met Lys Lys Ile Asp Val Lys Ile Leu Asp Pro Arg Val Gly Lys Glu Phe Pro Leu Pro Thr Tyr Ala Thr Ser Gly Ser Ala Gly Leu Asp Leu 20 Arg Ala Cys Leu Asn Asp Ala Val Glu Leu Ala Pro Gly Asp Thr Thr 40 Leu Val Pro Thr Gly Leu Ala Ile His Ile Ala Asp Pro Ser Leu Ala Ala Met Met Leu Pro Arg Ser Gly Leu Gly His Lys His Gly Ile Val Leu Gly Asn Leu Val Gly Leu Ile Asp Ser Asp Tyr Gln Gly Gln Leu Met Ile Ser Val Trp Asn Arg Gly Gln Asp Ser Phe Thr Ile Gln Pro Gly Glu Arg Ile Ala Gln Met Ile Phe Val Pro Val Val Gln Ala Glu 120 115 Phe Asn Leu Val Glu Asp Phe Asp Ala Thr Asp Arg Gly Glu Gly Gly 140 Phe Gly His Ser Gly Arg Gln 145 150 <210> 8 <211> 150 <212> PRT <213> Aquifex aeolicus <220> <223> deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase or Dut) (AAD)

10

Met Ser Lys Val Ile Leu Lys Ile Lys Arg Leu Pro His Ala Gln Asp

5

<400> 8

Leu Pro Leu Pro Ser Tyr Ala Thr Pro His Ser Ser Gly Leu Asp Leu 20 25 30

Arg Ala Ala Ile Glu Lys Pro Leu Lys Ile Lys Pro Phe Glu Arg Val 35 40 45

Leu Ile Pro Thr Gly Leu Ile Leu Glu Ile Pro Glu Gly Tyr Glu Gly
50 60

Gln Val Arg Pro Arg Ser Gly Leu Ala Trp Lys Lys Gly Leu Thr Val 65 70 75 80

Leu Asn Ala Pro Gly Thr Ile Asp Ala Asp Tyr Arg Gly Glu Val Lys 85 90 95

Val Ile Leu Val Asn Leu Gly Asn Glu Glu Val Val Ile Glu Arg Gly 100 105 110

Glu Arg Ile Ala Gln Leu Val Ile Ala Pro Val Gln Arg Val Glu Val 115 120 125

Val Glu Val Glu Glu Val Ser Gln Thr Gln Arg Gly Glu Gly Phe 130 135 140

Gly Ser Thr Gly Thr Lys 145 150

<210> 9

<211> 149

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:E. coli
 deoxyuridine 5'-triphosphate nucleotidohydrolase
 (dUTPase or Dut) (ECD) BlastP alignment sequence

<400> 9

Met Lys Lys Ile Asp Val Lys Ile Leu Asp Pro Arg Val Gly Lys Glu
1 5 10 15

Phe Pro Leu Pro Thr Tyr Ala Thr Ser Gly Ser Ala Gly Leu Asp Leu 20 25 30

Arg Ala Cys Leu Asn Asp Ala Val Glu Leu Ala Pro Gly Asp Thr Thr 35 40 45

Leu Val Pro Thr Gly Leu Ala Ile His Ile Ala Asp Pro Ser Leu Ala 50 55 60

Ala Met Met Leu Pro Arg Ser Gly Leu Gly His Lys His Gly Ile Val 65 70 75 80

Leu Gly Asn Leu Val Gly Leu Ile Asp Ser Asp Tyr Gln Gly Gln Leu
85 90 95

Met Ile Ser Val Trp Asn Arg Gly Gln Asp Ser Phe Thr Ile Gln Pro 100 105 110

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Gly Glu Arg Ile Ala Gln Met Ile Phe Val Pro Val Val Gln Ala Glu
115 120 125
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Phe Asn Leu Val Glu Asp Phe Asp Ala Thr Asp Arg Gly Glu Gly Gly 130 135

Phe Gly His Ser Gly 145

<210> 10

<211> 148

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Aquifex aeolicus deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase or Dut) (AAD) BlastP alignment sequence

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Met Ser Lys Val Ile Leu Lys Ile Lys Arg Leu Pro His Ala Gln Asp 1 5 10 15

Leu Pro Leu Pro Ser Tyr Ala Thr Pro His Ser Ser Gly Leu Asp Leu 20 25 30

Arg Ala Ile Glu Lys Pro Leu Lys Ile Lys Pro Phe Glu Arg Val

Leu Ile Pro Thr Gly Leu Ile Leu Glu Ile Pro Glu Gly Tyr Glu Gly 50 55 60

Gln Val Arg Pro Arg Ser Gly Leu Ala Trp Lys Lys Gly Leu Thr Val 65 70 75 80

Leu Asn Ala Pro Gly Thr Ile Asp Ala Asp Tyr Arg Gly Glu Val Lys 85 90 95

Val Ile Leu Val Asn Leu Gly Asn Glu Glu Val Val Ile Glu Arg Gly
100 105 110

Glu Arg Ile Ala Gln Leu Val Ile Ala Pro Val Gln Arg Val Glu Val
115 120 125

Val Glu Val Glu Glu Val Ser Gln Thr Gln Arg Gly Glu Gly Phe 130 135 140

Gly Ser Thr Gly 145

<210> 11

<211> 6 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus sequence

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<210> 12
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<223> Description of Artificial Sequence:consensus
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Pro Thr Gly Leu
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<400> 13
Pro Arg Ser Gly Leu
1
<210> 14
<211> 6
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:consensus
      sequence
<400> 14
Gly Glu Arg Ile Ala Gln
                  5
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<223> Description of Artificial Sequence:consensus
      sequence
<400> 15
Arg Gly Glu Gly Gly Phe Gly
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<210> 16
<211> 459
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence:consensus
      sequence, minimal encoding sequence using
      preferred E. coli codons
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atqarmaaar ttrwtstgaa aattmwgsrt cygcstswtg scmaagawtt wccgctgccg 60
asctatgcga ccyctsrcag ckcaggcctg gatctgcgtg cgkscmttra saawscgstg 120
raamttrmgc cgkktgawas grygctgrtt ccgaccggcc tgrycmttsa wattscggaw 180
ssttmtctgg mggsgmwgrt gckgccgcgt agcggcctgg scyrkaaama kggcwtaryg 240
stgskgaacs ygsygggcmy gattgatrsc gattatcrgg gcsaastgaw grttakcstg 300
kkgaacckgg gcmasgawkm akttrygatt sagcsgggcg aacgtattgc gcagmtgrtt 360
wttgygccgg tgswgcrggy ggaakttrwt swggtggaag awkttkmtsm gaccsakcgt 420
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<223> Description of Artificial Sequence:consensus
      sequence, minimal encoding sequence translation
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                                     10
Xaa Pro Leu Pro Xaa Tyr Ala Thr Xaa Xaa Ser Xaa Gly Leu Asp Leu
Arg Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Aro Xaa Xaa Xaa Xaa Xaa
Leu Xaa Pro Thr Gly Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa Leu Xaa
Xaa Xaa Xaa Pro Arg Ser Gly Leu Xaa Xaa Lys Xaa Gly Xaa Xaa
                     70
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```
Xaa Xaa Asn Xaa Xaa Gly Xaa Ile Asp Xaa Asp Tyr Xaa Gly Glx Xaa
Xaa Xaa Xaa Xaa Asn Xaa Gly Xaa Xaa Xaa Xaa Ile Glx Xaa
            100
                                105
Gly Glu Arg Ile Ala Gln Xaa Xaa Xaa Pro Val Xaa Xaa Glu
                            120
                                                125
Xaa Xaa Xaa Val Glu Xaa Xaa Xaa Xaa Thr Xaa Arg Gly Glu Gly Gly
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Phe Gly Xaa Xaa Gly Xaa Xaa
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      of non-similar degeneracies and selection of AAD
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asctatgcga ccyctcacag ckcaggcctg gatctgcgtg cgkscmttra saawscgstg 120
raamttrmqc cqkktqawas grygctgrtt ccgaccggcc tgatcmttsa wattscggaw 180
gqttmtqmqq sqcaqrtqck qccqcgtagc ggcctggsct ggaaamakgg cwtarygstg 240
ctgaacgcgs ygggcmygat tgatrscgat tatcrgggcs aastgawgrt takcstggtg 300
aacckqqqcm asgawgaakt trygattsag csgggcgaac gtattgcgca gmtgrttwtt 360
gygccggtgs wgcrggygga akttrwtswg gtggaagawk tttctcagac csakcgtggc 420
gaaggcggct ttggctctas cggcasamag taatga
<210> 19
<211> 150
<212> PRT
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                                      10
Xaa Pro Leu Pro Xaa Tyr Ala Thr Xaa His Ser Xaa Gly Leu Asp Leu
                                  25
             20
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- Arg Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa 35 40 45
- Leu Xaa Pro Thr Gly Leu Ile Xaa Xaa Ile Xaa Xaa Gly Xaa Xaa Xaa 50 55 60
- Gln Xaa Xaa Pro Arg Ser Gly Leu Xaa Trp Lys Xaa Gly Xaa Xaa Xaa 65 70 75 80
- Leu Asn Ala Xaa Gly Xaa Ile Asp Xaa Asp Tyr Xaa Gly Glx Xaa Xaa 85 90 . 95
- Xaa Xaa Xaa Asn Asn Xaa Gly Xaa Xaa Glu Xaa Xaa Ile Glx Xaa Gly
 100 105 110
- Glu Arg Ile Ala Gln Xaa Xaa Xaa Pro Val Xaa Xaa Xaa Glu Xaa 115 120 125
- Xaa Xaa Val Glu Xaa Xaa Ser Gln Thr Xaa Arg Gly Glu Gly Gly Phe 130 135 140
- Gly Ser Xaa Gly Xaa Xaa 145 150
- <210> 20
- <211> 487
- <212> DNA
- <213> Artificial Sequence
- <220>
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- <400> 20
 ttggtaccaa gcttcatatg armaaarttr wtstgaaaat tmwgcgtcyg cstcatgscm 60
 aagawttwcc gctgccgasc tatgcgaccy ctcacagckc aggcctggat ctgcgtgcgk 120
 scmttrasra wscgstgraa mttrmgccgk ktgawasgry gctgrttccg accggtctga 180
 tcmttsawat tscggawggt tmtgmggsgc agrtgckgcc gcgtagcggc ctggsctgga 240
 aamakggcwt arygstgctg aacgcgsygg gcmygatcga trscgattat crgggcsaas 300
 tgawgrttak cstggtgaac ckgggcmasg awgaakttry gattsagcsg ggcgaacgta 360
 ttgcgcagmt grttwttgyg ccggtgswgc rggyggaakt trwtswggtg gaagawkttt 420
 ctcagaccsa kcgtggcgaa ggcgctttg gctctascgg casamagtaa tgaggatccg 480
 aattctt
- <210> 21
- <211> 150
- <212> PRT
- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence:consensus sequence, minimal encoding sequence translation after removal of non-similar degeneracies and selection of AAD parent residues

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Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile
         35
                              40
Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg
Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile
                     70
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Asp Ile Pro		Lys A	rg Tyr 120	Leu	Ile	Asp	Lys	Gly 125	Leu	Ile	Pro
Met Glu Gly 130	Xaa Glu		eu Lys 35	Xaa	Leu	Ala	Phe 140	Asp	Ile	Glu	Thr
Leu Tyr His 145	Glu Gly	Glu·G 150	lu Phe	Xaa	Lys	Gly 155	Pro	Ile	Ile	Met	Ile 160
Ser Tyr Ala	Asp Glu 165		lu Ala	Lys	Val 170	Ile	Thr	Trp	Lys	Xaa 175	Ile
Asp Leu Pro	Tyr Val 180	Glu V	al Val	Ser 185	Ser	Glu	Arg	Glu	Met 190	Ile	Lys
Arg Phe Leu 195		Ile A	rg Glu 200	Lys	Asp	Pro	Asp	Xaa 205	Ile	Xaa	Thr
Tyr Asn Gly 210	Asp Ser		sp Xaa 15	Pro	Tyr	Leu	Xaa 220	Lys	Arg	Ala	Glu
Lys Leu Gly 225	lle Lys	Leu X	aa Xaa	Gly	Arg	Asp 235	Gly	Ser	Glu	Pro	Lys 240
Met Gln Arg	Xaa Gly 245		et Thr	Ala	Val 250	Glu	Xaa	Lys	Gly	Arg 255	Ile
His Phe Asp	Leu Tyr 260	His V	al Ile	Xaa 265	Arg	Thr	Ile	Asn	Leu 270	Pro	Thr
Tyr Thr Let 275		Val T	yr Glu 280	Ala	Ile	Phe	Gly	Lys 285	Pro	Lys	Glu
Lys Val Tyr 290	· Ala Xaa		le Ala 95	Xaa	Ala	Trp	Glu 300	Xaa	Gly	Xaa	Xaa
Leu Glu Arg 305	Val Ala	Lys T	yr Ser	Met	Glu	Asp 315	Ala	Lys	Xaa	Thr	Tyr 320
Glu Leu Gly	Xaa Glu 325		aa Pro	Met	Glu 330	Xaa	Gln	Leu	Ser	Arg 335	Leu
Val Gly Glr	Pro Leu 340	Trp A	sp Val	Ser 345	Arg	Ser	Ser	Thr	Gly 350	Asn	Leu
Val Glu Trp 355		Leu A	rg Lys 360	Ala	Tyr	Glu	Arg	Asn 365	Glu	Xaa	Ala
Pro Asn Lys 370	Pro Xaa		aa Glu 75	Tyr	Glx	Arg	Arg 380	Leu	Arg	Glu	Ser
Tyr Xaa Gly	Glv Xaa	Val I	vs Glu	Pro	Glu	Lvs	Glv	Leu	Trn	Glu	Yaa

Xaa Val Xaa Leu Asp Phe Arg Xaa Leu Tyr Pro Ser Ile Ile Ile Thr 405 410 His Asn Val Ser Pro Asp Thr Leu Asn Xaa Glu Gly Cys Xaa Xaa Tyr 425 Asp Xaa Ala Pro Glx Val Gly His Lys Phe Cys Lys Asp Xaa Pro Gly 440 Phe Ile Pro Ser Leu Leu Xaa Xaa Leu Leu Xaa Glu Arg Gln Xaa Ile 455 Lys Xaa Lys Met Lys Xaa Xaa Xaa Asp Pro Ile Glu Lys Xaa Xaa Leu 475 Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly 490 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu 520 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly 530 Leu Tyr Ala Thr Ile Pro Gly Xaa Xaa Xaa Glu Glu Ile Lys Lys 550 555 Ala Leu Glu Phe Val Lys Tyr Ile Asn Xaa Lys Leu Pro Gly Leu Leu 565 570 Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly Phe Phe Val Thr Lys Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys Xaa Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly Asx Val Glu Glu Ala 635 Val Xaa Ile Val Lys Glu Val Xaa Glx Lys Leu Xaa Xaa Tyr Glu Ile 650 Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile Thr Arg Pro Leu His 665 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Xaa Leu Ala 680 Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val Ile Gly Tyr Ile Val 695 700 Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala Ile Leu Ala Glu Glu 705 710 715 720

Xaa Asp Xaa Xaa Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Xaa Phe Gly Tyr Arg 740 745 750

Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln Xaa Gly Leu Thr Xaa 755 760 765

Trp Leu Asn Ile Lys Lys Ser Gly Thr His
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20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile 35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg 50 55 60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile 65 70 75 80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Gly Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr 195 200 205

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Lys 225	Leu	Gly	Ile	Lys	Leu 230	Thr	Ile	Gly	Arg	Asp 235	Gly	Ser	Glu	Pro	Lys 240
Met	Gln	Arg	Ile	Gly 245	Asp	Met	Thr	Ala	Val 250	Glu	Val	Lys	Gly	Arg 255	Ile
His	Phe	Asp	Leu 260	Tyr	His	Val	Ile	Thr 265	Arg	Thr	Ile	Asn	Leu 270	Pro	Thr
Tyr	Thr	Leu 275	Glu	Ala	Val	Tyr	Glu 280	Ala	Ile	Phe	Gly	Lys 285	Pro	Lys	Glu
Lys	Val 290	Tyr	Ala	Asp	Glu	Ile 295	Ala	Lys	Ala	Trp	Glu 300	Ser	Gly	Glu	Asn
Leu 305	Glu	Arg	Val	Ala	Lys 310	Tyr	Ser	Met	Glu	Asp 315	Ala	Lys	Ala	Thr	Tyr 320
Glu	Leu	Gly	Lys	Glu 325	Phe	Leu	Pro	Met	Glu 330	Ile	Gln	Leu	Ser	Arg 335	Leu
Val	Gly	Gln	Pro 340	Leu	Trp	Asp	Val	Ser 345	Arg	Ser	Ser	Thr	Gly 350	Asn	Leu
Val	Glu	Trp 355	Phe	Leu	Leu	Arg	Lys 360	Ala	Tyr	Glu	Arg	Asn 365	Glu	Val	Ala
Pro	Asn	Lys	Pro	Ser	Glu	Glu	Glu	Tyr	Gln	Arg	Arg	Leu	Arg	Glu	Ser
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Tyr 385		Gly	Gly	Phe	Val 390		Glu	Pro	Glu	Lys 395		Leu	Trp	Glu	Asn 400
385	Thr				390	Lys				395	Gly		Trp		400
385 Ile	Thr Val	Tyr	Leu	Asp 405	390 Phe	Lys Arg	Ala	Leu	Tyr 410	395 Pro	Gly Ser	Ile		Ile 415	400 Thr
385 Ile His	Thr Val Asn	Tyr Val	Leu Ser 420	Asp 405 Pro	390 Phe Asp	Lys Arg Thr	Ala Leu	Leu Asn 425	Tyr 410 Leu	395 Pro Glu	Gly Ser Gly	Ile Cys	Ile Lys 430	Ile 415 Asn	400 Thr
385 Ile His	Thr Val Asn Ile	Tyr Val Ala 435	Leu Ser 420 Pro	Asp 405 Pro Gln	390 Phe Asp Val	Lys Arg Thr	Ala Leu His 440	Leu Asn 425 Lys	Tyr 410 Leu Phe	395 Pro Glu Cys	Gly Ser Gly Lys	Ile Cys Asp 445	Ile Lys 430	Ile 415 Asn Pro	400 Thr Tyr Gly
385 Ile His Asp	Thr Val Asn Ile Ile 450	Tyr Val Ala 435 Pro	Leu Ser 420 Pro	Asp 405 Pro Gln Leu	390 Phe Asp Val Leu	Lys Arg Thr Gly Gly 455	Ala Leu His 440	Leu Asn 425 Lys Leu	Tyr 410 Leu Phe Leu	395 Pro Glu Cys Glu	Gly Ser Gly Lys Glu 460	Ile Cys Asp 445 Arg	Ile Lys 430 Ile	Ile 415 Asn Pro	400 Thr Tyr Gly Ile
385 Ile His Asp Phe Lys 465	Thr Val Asn Ile Ile 450 Thr	Tyr Val Ala 435 Pro	Leu Ser 420 Pro Ser	Asp 405 Pro Gln Leu Lys	390 Phe Asp Val Leu Glu 470	Lys Arg Thr Gly Gly 455 Thr	Ala Leu His 440 His	Leu Asn 425 Lys Leu Asp	Tyr 410 Leu Phe Leu	395 Pro Glu Cys Glu Ile 475	Gly Ser Gly Lys Glu 460	Ile Cys Asp 445 Arg	Ile Lys 430 Ile Gln	Ile 415 Asn Pro Lys Leu	400 Thr Tyr Gly Ile Leu 480
385 Ile His Asp Phe Lys 465 Asp	Thr Val Asn Ile Ile 450 Thr	Tyr Val Ala 435 Pro Lys Arg	Leu Ser 420 Pro Ser Met	Asp 405 Pro Gln Leu Lys 485	390 Phe Asp Val Leu Glu 470 Ala	Lys Arg Thr Gly Gly 455 Thr	Ala Leu His 440 His Gln	Leu Asn 425 Lys Leu Asp	Tyr 410 Leu Phe Leu Pro	395 Pro Glu Cys Glu Ile 475 Ala	Gly Ser Gly Lys Glu 460 Glu Asn	Ile Cys Asp 445 Arg Lys	Ile Lys 430 Ile Gln	Ile 415 Asn Pro Lys Leu Tyr 495	400 Thr Tyr Gly Ile Leu 480 Gly

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly 535 Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys 550 555 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu 570 565 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys 585 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly 600 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln 615 Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala 630 Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile 650 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala 680 Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn. Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser Trp Leu Asn Ile Lys Lys Ser 770 <210> 25 <211> 775 <212> PRT <213> Artificial Sequence <223> Description of Artificial Sequence:parent Pyrococcus sp. GD-B (Deep Vent) DNA polymerase

10

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile

5

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg 25 Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Gln Ile 40 Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile Glu Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile Arg Asp Lys Ile Arg Glu His Ser Ala Val Ile Asp Ile Phe Glu Tyr Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 135 Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 170 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Val Ile Ile Thr Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Val Lys Arg Ala Glu 215 Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile 245 250 His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr 265 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 280 285 Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Thr Gly Lys Gly 295 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr 310 315 Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu 325 330 335

vai	Gly	Gln	Pro 340	Leu	Trp	Asp	Val	Ser 345	Arg	Ser	Ser	Thr	Gly 350	Asn	Leu
Val	Glu	Trp 355	Tyr	Leu	Leu	Arg	Lys 360	Ala	Tyr	Glu	Arg	Asn 365	Glu	Leu	Ala
Pro	Asn 370	Lys	Pro	Asp	Glu	Arg 375	Glu	Tyr	Glu	Arg	Arg 380	Leu	Arg	Glu	Ser
Tyr 385	Ala	Gly	Gly	Tyr	Val 390	Lys	Glu	Pro	Glu	Lys 395	Gly	Leu	Trp	Glu	Gly 400
Leu	Val	Ser	Leu	Asp 405	Phe	Arg	Ser	Leu	Tyr 410	Pro	Ser	Ile	Ile	Ile 415	Thr
His	Asn	Val	Ser 420	Pro	Asp	Thr	Leu	Asn 425	Arg	Glu	Gly	Cys	Arg 430	Glu	Tyr
Asp	Val	Ala 435	Pro	Glu	Val	Gly	His 440	Lys	Phe	Cys	Lys	Asp 445	Phe	Pro	Gly
Phe	Ile 450	Pro	Ser	Leu	Leu	Lys 455	Arg	Leu	Leu	Asp	Glu 460	Arg	Gln	Glu	Ile
Lys 465	Arg	Lys	Met	Lys	Ala 470	Ser	Lys	Asp	Pro	Ile 475	Glu	Lys	Lys	Met	Leu 480
Asp	Tyr	Arg	Gln	Arg 485	Ala	Ile	Lys	Ile	Leu 490	Ala	Asn	Ser	Tyr	Tyr 495	Gly
Tyr	Tyr	Gly	Tyr 500	Ala	Lys	Ala	Arg	Trp 505	Tyr	Cys	Lys	Glu	Cys 510	Ala	Glu
Ser	Val	Thr 515	Ala	Trp	Gly	Arg	Glu 520	Tyr	Ile	Glu	Phe	Val 525	Arg	Lys	Glu
		515					520					525			Glu Gly
Leu	Glu 530	515 Glu	Lys	Phe	Gly	Phe 535	520 Lys	Val	Leu	Tyr	Ile 540	525 Asp	Thr		Gly
Leu Leu 545	Glu 530 Tyr	515 Glu Ala	Lys Thr	Phe Ile	Gly Pro 550	Phe 535 Gly	520 Lys Ala	Val Lys	Leu Pro	Tyr Glu 555	Ile 540 Glu	525 Asp Ile	Thr Lys	Asp	Gly Lys 560
Leu Leu 545 Ala	Glu 530 Tyr Leu	515 Glu Ala Glu	Lys Thr	Phe Ile Val 565	Gly Pro 550 Asp	Phe 535 Gly Tyr	520 Lys Ala Ile	Val Lys Asn	Leu Pro Ala 570	Tyr Glu 555 Lys	Ile 540 Glu Leu	525 Asp Ile Pro	Thr Lys Gly	Asp Lys Leu	Gly Lys 560 Leu
Leu Leu 545 Ala Glu	Glu 530 Tyr Leu Leu	515 Glu Ala Glu	Lys Thr Phe Tyr 580	Phe Ile Val 565	Gly Pro 550 Asp	Phe 535 Gly Tyr	520 Lys Ala Ile Tyr	Val Lys Asn Val	Leu Pro Ala 570 Arg	Tyr Glu 555 Lys Gly	Ile 540 Glu Leu Phe	525 Asp Ile Pro	Thr Lys Gly Val	Asp Lys Leu 575	Gly Lys 560 Leu Lys
Leu Leu 545 Ala Glu Lys	Glu 530 Tyr Leu Leu	515 Glu Ala Glu Glu Tyr 595	Lys Thr Phe Tyr 580 Ala	Phe Ile Val 565 Glu Leu	Gly Pro 550 Asp Gly Ile	Phe 535 Gly Tyr Phe Asp	520 Lys Ala Ile Tyr Glu 600	Val Lys Asn Val 585 Glu	Leu Pro Ala 570 Arg	Tyr Glu 555 Lys Gly Lys	Ile 540 Glu Leu Phe Ile	S25 Asp Ile Pro Phe Ile 605	Thr Lys Gly Val 590	Asp Lys Leu 575 Thr	Gly Lys 560 Leu Lys
Leu 545 Ala Glu Lys Leu	Glu 530 Tyr Leu Leu Lys Glu 610	S15 Glu Ala Glu Glu Tyr 595 Ile	Lys Thr Phe Tyr 580 Ala	Phe Ile Val 565 Glu Leu Arg	Gly Pro 550 Asp Gly Ile Arg	Phe 535 Gly Tyr Phe Asp 615	520 Lys Ala Ile Tyr Glu 600 Trp	Val Lys Asn Val 585 Glu Ser	Leu Pro Ala 570 Arg Gly	Tyr Glu 555 Lys Gly Lys	Ile 540 Glu Leu Phe Ile Ala 620	Asp Ile Pro Phe Ile 605 Lys	Thr Lys Gly Val 590 Thr	Asp Lys Leu 575 Thr	Gly Lys 560 Leu Lys Gly

Pro Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660 665 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala 675 680 685

Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val 690 695 700

Leu Arg Gly Asp Gly Pro Ile Ser Lys Arg Ala Ile Leu Ala Glu Glu 705 · 710 715 720

Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
740 745 750

Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Thr Gly Leu Thr Ala 755 760 765

Trp Leu Asn Ile Lys Lys Lys
770 775

<210> 26

<211> 783

<212> PRT

<213> Artificial Sequence

<220×

<223> Description of Artificial Sequence:designed hybrid
 polymerase from Figure 11

<220>

<221> MOD_RES

<222> (1)..(783)

<223> Xaa = unknown amino acid

<400> 26

Met Ile Leu Asp Xaa Asp Tyr Ile Thr Glu Xaa Gly Lys Pro Xaa Ile 1 5 10 15

Arg Xaa Phe Lys Lys Glu Asn Gly Xaa Phe Lys Xaa Glu Xaa Asp Arg 20 25 30

Xaa Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Xaa Asp Asp Ser Xaa Ile 35 40 45

Xaa Glu Val Xaa Lys Ile Thr Xaa Glu Arg His Gly Lys Ile Val Arg 50 55 60

Ile Xaa Asp Xaa Glu Lys Val Xaa Lys Lys Phe Leu Gly Xaa Pro Ile 65 70 75 80

Xaa Val Trp Xaa Leu Tyr Xaa Glu His Pro Gln Asp Val Pro Xaa Ile 85 90 95

Arg Xaa Lys Xaa Arg Glu His Xaa Ala Val Xaa Asp Ile Phe Glu Tyr 100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 Met Glu Gly Xaa Glu Glu Leu Lys Xaa Leu Ala Phe Asp Ile Glu Thr Leu Tyr His Glu Gly Glu Phe Xaa Lys Gly Pro Ile Ile Met Ile Ser Tyr Ala Asp Glu Xaa Glu Ala Lys Val Ile Thr Trp Lys Xaa Ile 170 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys Arg Phe Leu Xaa Xaa Ile Arg Glu Lys Asp Pro Asp Xaa Ile Xaa Thr 200 Tyr Asn Gly Asp Ser Phe Asp Xaa Pro Tyr Leu Xaa Lys Arg Ala Glu 215 Lys Leu Gly Ile Lys Leu Xaa Xaa Gly Arg Asp Gly Ser Glu Pro Lys 230 235 Met Gln Arg Xaa Gly Asp Met Thr Ala Val Glu Xaa Lys Gly Arg Ile His Phe Asp Leu Tyr His Val Ile Xaa Arg Thr Ile Asn Leu Pro Thr 265 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu Lys Val Tyr Ala Xaa Glu Ile Ala Xaa Ala Trp Glu Xaa Gly Xaa Xaa Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Xaa Thr Tyr 310 315 Glu Leu Gly Xaa Glu Phe Xaa Pro Met Glu Xaa Gln Leu Ser Arg Leu 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu 350 345 Val Glu Trp Xaa Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Xaa Ala 360 Pro Asn Lys Pro Xaa Glu Xaa Glu Tyr Xaa Arg Arg Leu Arg Glu Ser 370 375 380 Tyr Xaa Gly Gly Xaa Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Xaa 390 Xaa Val Xaa Leu Asp Phe Arg Xaa Leu Tyr Pro Ser Ile Ile Ihr 410 His Asn Val Ser Pro Asp Thr Leu Asn Xaa Glu Gly Cys Xaa Xaa Tyr 420 425 430

Asp Xaa Ala Pro Xaa Val Gly His Lys Phe Cys Lys Asp Xaa Pro Gly 440 435 Phe Ile Pro Ser Leu Leu Xaa Xaa Leu Leu Xaa Glu Arg Gln Xaa Ile 455 Lys Xaa Lys Met Lys Xaa Xaa Xaa Asp Pro Ile Glu Lys Xaa Xaa Leu 470 475 Asp Tyr Arg Gln Xaa Ala Ile Lys Xaa Leu Ala Asn Ser Xaa Tyr Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser Val Thr Ala Trp Gly Arg Xaa Tyr Ile Glu Xaa Val Xaa Lys Glu 520 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly Leu Tyr Ala Thr Ile Pro Gly Xaa Xaa Kaa Glu Glu Ile Lys Lys 550 555 Ala Leu Glu Phe Val Lys Tyr Ile Asn Xaa Lys Leu Pro Gly Leu Leu 570 Glu Leu Glu Tyr Glu Gly Phe Tyr Xaa Arg Gly Phe Phe Val Thr Lys 585 Lys Xaa Tyr Ala Xaa Ile Asp Glu Glu Gly Lys Xaa Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala Xaa Val Leu Glu Xaa Ile Leu Lys His Gly Xaa Val Glu Glu Ala 630 Val Xaa Ile Val Lys Glu Val Xaa Xaa Lys Leu Xaa Xaa Tyr Glu Ile Pro Pro Glu Lys Leu Xaa Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Xaa Leu Ala 680 Ala Xaa Gly Val Lys Xaa Xaa Pro Gly Met Val Ile Gly Tyr Ile Val 690 695 Leu Arg Gly Asp Gly Pro Ile Ser Xaa Arg Ala Ile Leu Ala Glu Glu 710 715 Xaa Asp Xaa Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 730 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Xaa Phe Gly Tyr Arg 740 745 750

Lys Glu Asp Leu Arg Xaa Gln Lys Thr Xaa Gln Xaa Gly Leu Thr Xaa 755 760 765

Trp Leu Asn Ile Lys Lys Ser Gly Thr His Asn Cys Asn His Asp 770 775 780

<210> 27

<211> 845

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid polymerase HyS1 from Figure 11

<220>

<221> MOD RES

<222> (472)

<223> Xaa = unknown amino acid

<400> 27

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile 1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg
20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
35 40 45

Glu Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Val Asp Val Glu Lys Val Arg Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80

Lys Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95

Arg Asp Lys Val Arg Glu His Pro Ala Val Ile Asp Ile Phe Glu Tyr 100 105 110

Asp Ile Ala Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Gly Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Gly Ser Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr 195 200 205

Tyr	Asn 210	Gly	Asp	Ser	Phe	Asp 215	Leu	Pro	Tyr	Leu	Ala 220	Lys	Arg	Ala	Glu
Lys 225	Leu	Gly	Ile	Lys	Leu 230	Thr	Leu	Gly	Arg	Asp 235	Gly	Cys	Glu	Ala	Lys 240
Met	Gln	Arg	Leu	Gly 245	Asp	Met	Thr	Ala	Val 250	Glu	Val	Lys	Gly	Arg 255	Ile
His	Phe	Asp	Leu 260	Tyr	Tyr	Val	Ile	Ser 265	Arg	Thr	Ile	Asn	Leu 270	Pro	Thr
Tyr	Thr	Leu 275	Glu	Ala	Val	Tyr	Glu 280	Ala	Ile	Phe	Gly	Lys 285	Pro	Lys	Glu
Lys	Val 290	Tyr	Ala	Asp	Asp	Ile 295	Ala	Glu	Ala	Trp	Glu 300	Thr	Gly	Lys	Gly
Leu 305	Glu	Arg	Val	Ala	Lys 310	Tyr	Ser	Met	Glu	Asp 315	Ala	Lys	Ala	Thr	Tyr 320
Glu	Leu	Gly	Lys	Glu 325	Phe	Leu	Pro	Met	Glu 330	Ala	Gln	Leu	Ser	Arg 335	Leu
Val	Gly	Gln	Pro 340	Leu	Trp	Asp	Val	Ser 345	Arg	Ser	Ser	Thr	Gly 350	Asn	Leu
Val	Glu	Trp 355	Tyr	Leu	Leu	Arg	Lys 360	Ala	Tyr	Glu	Arg	Asn 365	Glu	Val	Ala
Pro	Asn 370	Lys	Pro	Tyr	Glu	Arg 375	Glu	Tyr	Glu	Arg	Arg 380	Leu	Arg	Glu	Ser
Tyr 385	Thr	Gly	Gly	Phe	Val 390	Lys	Glu	Pro	Glu	Lys 395	Gly	Leu	Trp	Glu	Ser 400
Leu	Val	Ser	Leu	Asp 405	Phe	Arg	Ser	Leu	Tyr 410	Pro	Ser	Ile	Ile	Ile 415	Thr
His	Asn	Val	Ser 420	Pro	Asp	Thr	Leu	Asn 425	Arg	Glu	Gly	Cys	Lys 430	Asp	Tyr
Asp	Ile	Ala 435	Pro	Glu	Val	Gly	His 440	Lys	Phe	Cys	Lys	Asp 445	Phe	Leu	Gly
Phe	Ile 450	Pro	Ser	Leu	Leu	Gly 455	His	Leu	Leu	Glu	Glu 460	Arg	Gln	Glu	Ile
Lys 465	Thr	Lys	Met	Lys	Glu 470	Thr	Xaa	Asp	Pro	Ile 475	Glu	Lys	Ile	Leu	Leu 480
Asp	Tyr	Arg	Gln	Lys 485	Ala	Ile	Lys	Leu	Leu 490	Ala	Asn	Ser	Tyr	Tyr 495	Gly
Tyr	Tyr	Gly	Tyr 500	Ala	Lys	Ala	Arg	Trp 505	Tyr	Cys	Lys	Glu	Cys 510	Ala	Glu
Ser	Val	Thr 515	Ala	Trp	Gly	Arg	Glu 520	Tyr	Ile	Glu	Phe	Val 525	Trp	Lys	Glu

Leu	Glu 530	Glu	Lys	Phe	Gly	Phe 535	Lys	Val	Leu	Tyr	Ile 540	Asp	Thr	Asp	Gly
Leu 545	Tyr	Ala	Thr	Ile	Pro 550	Gly	Gly	Glu	Pro	Glu 555	Glu	Ile	Lys	Lys	Lys 560
Ala	Leu	Glu	Phe	Val 565	Lys	Tyr	Ile	Asn	Ser 570	Lys	Leu	Pro	Gly	Leu 575	Leu
Glu	Leu	Glu	Tyr 580	Glu	Gly	Phe	Tyr	Lys 585	Arg	Gly	Phe	Phe	Val 590	Thr	Lys
Lys	Arg	Tyr 595	Ala	Val	Ile	Asp	Glu 600	Glu	Gly	Lys	Ile	Ile 605	Thr	Arg	Gly
Leu	Glu 610	Ile	Val	Arg	Arg	Asp 615	Trp	Ser	Glu	Ile	Ala 620	Lys	Glu	Thr	Gln
Ala 625	Lys	Val	Leu	Glu	Ala 630	Ile	Leu	Lys	His	Gly 635	Asn	Val	Glu	Glu	Ala 640
Val	Lys	Ile	Val	Lys 645	Glu	Ile	Ile	Glu	Lys 650	Leu	Ala	Lys	Tyr	Glu 655	Ile
Pro	Pro	Glu	Lys 660	Leu	Ala	Ile	Tyr	Glu 665	Gln	Ile	Thr	Arg	Pro 670	Leu	His
Glu	Tyr	Lys 675	Ala	Ile	Gly	Pro	His 680	Val	Ala	Val	Ala	Lys 685	Lys	Leu	Ala
Ala	Arg 690	Gly	Val	Lys	Ile	Lys 695	Pro	Gly	Met	Val	Ile 700	Gly	Tyr	Ile	Val
Leu 705	Arg	Gly	Asp	Gly	Pro 710	Ile	Ser	Lys	Arg	Ala 715	Ile	Leu	Ala	Glu	Glu 720
Phe	Asp	Pro	Lys	Lys 725	His	Lys	Tyr	Asp	Ala 730	Glu	Tyr	Tyr	Ile	Glu 735	Asn
Gln	Val	Leu	Pro 740	Ala	Val	Leu	Arg	Ile 745	Leu	Glu	Gly	Phe	Gly 750	Tyr	Arg
Lys	Glu	Asp 755	Leu	Arg	Trp	Gln	Lys 760	Thr	Lys	Gln	Ala	Gly 765	Leu	Thr	Ala
Trp	Leu 770	Asn	Ile	Lys	Lys	Ser 775	Gly	Thr	Gly	Gly	Gly 780	Gly	Ala	Thr	Val
Lys 785	Phe	Lys	Tyr	Lys	Gly 790	Glu	Glu	Lys	Glu	Val 795	Asp	Ile	Ser	Lys	Ile 800
Lys	Lys	Val	Trp	Arg 805	Val	Gly	Lys	Met	Ile 810	Ser	Phe	Thr	Tyr	Asp 815	Glu
Gly	Gly	Gly	Lys 820	Thr	Gly	Arg	Gly	Ala 825	Val	Ser	Glu	Lys	Asp 830	Ala	Pro
Lys	Glu	Leu 835	Leu	Gln	Met	Leu	Glu 840	Lys	Gln	Lys	Lys	Asn 845			

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<210> 28
<211> 758
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:hybrid
     polymerase Hyb2 from Figure 11
<220>
<221> MOD RES
<222> (472)
<223> Xaa = unknown amino acid
<400> 28
Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile
Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr
                                105
Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
Met Glu Gly Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr
Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile
145
                    150
Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
                                185
            180
Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr
                            200
Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu
```

235

215

230

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys

210

225

Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile 250 245 His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr 265 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 280 Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp 295 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala 360 Pro Asn Lys Pro Ala Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser 375 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp 390 395 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ihr His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile 455 Lys Thr Lys Met Lys Glu Thr Xaa Asp Pro Ile Glu Lys Ile Leu Leu 465 470 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Tyr Tyr Gly 490 485 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 505 500 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu 520 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly 535 540 Leu Tyr Ala Thr Ile Pro Gly Gly Glu Pro Glu Glu Ile Lys Lys 545 550 555 560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu 570 565 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys 585 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly 600 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln 620 Ala Lys Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala Val Lys Ile Val Lys Glu Ile Ile Glu Lys Leu Ala Lys Tyr Glu Ile Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala 680 Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val 690 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu 710 715 Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg Lys Glu Asp Leu Arg Asn 755 <210> 29 <211> 758 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence:hybrid polymerase Hyb3 from Figure 11 <220> <221> MOD RES <222> (472) <223> Xaa = unknown amino acid Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile

30

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg

25

20

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile 40 Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro Met Glu Gly Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr Leu Tyr His Glu Gly Glu Phe Ala Lys Gly Pro Ile Ile Met Ile 150 Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 185 Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile 250 His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr 260 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp 295 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr 310 315 Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu 325 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu 340 345 350

		_	_	_	_	_	_		_	~ 3	_	_	~ 7	.	.
Val	Glu	Trp 355	Leu	Leu	Leu	Arg	160	Ala	Tyr	Glu	Arg	Asn 365	Glu	Leu	Ala
Pro	Asn 370	Lys	Pro	Ala	Glu	Gln 375	Glu	Tyr	Glu	Arg	Arg 380	Leu	Arg	Glu	Ser
Tyr 385	Thr	Gly	Gly	Phe	Val 390	Lys	Glu	Pro	Glu	Lys 395	Gly	Leu	Trp	Glu	Asp 400
Leu	Val	Ser	Leu	Asp 405	Phe	Arg	Ala	Leu	Tyr 410	Pro	Ser	Ile	Ile	Ile 415	Thr
His	Asn	Val	Ser 420	Pro	Asp	Thr	Leu	Asn 425	Arg	Glu	Gly	Cys	Lys 430	Asp	Tyr
Asp	Ile	Ala 435	Pro	Glu	Val	Gly	His 440	Lys	Phe	Cys	Lys	Asp 445	Phe	Leu	Gly
Phe	Ile 450	Pro	Ser	Leu	Leu	Gly 455	His	Leu	Leu	Glu	Glu 460	Arg	Gln	Glu	Ile
Lys 465	Thr	Lys	Met	Lys	Glu 470	Thr	Xaa	Asp	Pro	Ile 475	Glu	Lys	Ile	Leu	Leu 480
Asp	Tyr	Arg	Gln	Lys 485	Ala	Ile	Lys	Leu	Leu 490	Ala	Asn	Ser	Tyr	Tyr 495	Gly
Tyr	Tyr	Gly	Tyr 500	Ala	Lys	Ala	Arg	Trp 505	Tyr	Cys	Lys	Glu	Cys 510	Ala	Glu
Ser	Val	Thr 515	Ala	Trp	Gly	Arg	Glu 520	Tyr	Ile	Glu	Phe	Val 525	Trp	Lys	Glu
Leu	Glu 530	Glu	Lys	Phe	Gly	Phe 535	Lys	Val	Leu	Tyr	Ile 540	Asp	Thr	Asp	Gly
Leu 545	Tyr	Ala	Thr	Ile	Pro 550	Gly	Gly	Glu	Pro	Glu 555	Glu	Ile	Lys	Lys	Lys 560
Ala	Leu	Glu	Phe	Val 565	Lys	Tyr	Ile	Asn	Ser 570	Lys	Leu	Pro	Gly	Leu 575	Leu
Glu	Leu	Glu	Tyr 580	Glu	Gly	Phe	Tyr	Lys 585	Arg	Gly	Phe	Phe	Val 590	Thr	Lys
Lys	Arg	Tyr 595	Ala	Val	Ile	Asp	Glu 600	Glu	Gly	Lys	Ile	Ile 605	Thr	Arg	Gly
Leu	Glu 610	Ile	Val	Arg	Arg	Asp 615	Trp	Ser	Glu	Ile	Ala 620	Lys	Glu	Thr	Gln
Ala 625	Lys	Val	Leu	Glu	Ala 630	Ile	Leu	Lys	His	Gly 635	Asn	Val	Glu	Glu	Ala 640
Val	Lys	Ile	Val	Lys 645	Glu	Ile	Ile	Glu	Lys 650	Leu	Ala	Lys	Tyr	Glu 655	Ile
Pro	Pro	Glu	Lys 660	Leu	Ala	Ile	Tyr	Glu 665	Gln	Ile	Thr	Arg	Pro 670	Leu	His

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala 675 680 685

Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val 690 695 . 700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu 705 710 715 720

Phe Asp Leu Arg Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
740 745 750

Lys Glu Asp Leu Arg Asn 755

<210> 30

<211> 845

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid polymerase HyS4 from Figure 11

<220>

<221> MOD RES

<222> (472)

<223> Xaa = unknown amino acid

<400> 30

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile 1 5 10 15

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg 20 25 30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Glu Asp Asp Ser Lys Ile 35 40 45

Asp Glu Val Arg Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile 65 70 75 80

Thr Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Gly Ile Phe Glu Tyr 100 105 110

Asp Ile Pro Phe Ala Lys Ser Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Ala Lys Gly Pro Ile Ile Met Ile 150 Ser Tyr Ala Asp Glu Asp Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 165 170 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 185 Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Val Ile Val Thr Tyr Asn Gly Asp Ser Phe Asp Leu Pro Tyr Leu Ala Lys Arg Ala Glu Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys 230 Met Gln Arg Leu Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile His Phe Asp Leu Tyr His Val Ile Ser Arg Thr Ile Asn Leu Pro Thr 265 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 280 Lys Val Tyr Ala Asp Glu Ile Ala Gly Ala Trp Glu Thr Gly Glu Asp Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Ile Tyr Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Val Gln Leu Pro Arg Leu Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala 360 Pro Asn Lys Pro Ala Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser 370 380 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asp 390 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ihr 405 410 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Asp Tyr 425 Asp Ile Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Leu Gly 440 445 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Glu Ile 450 455 460

Lys Thr Lys 465	Met Lys	Glu 7 470	Thr Xaa	Asp	Pro	Ile 475	Glu	Lys	Ile	Leu	Leu 480
Asp Tyr Arg	Gln Lys 485	Ala 1	Ile Lys	Leu	Leu 490	Ala	Asn	Ser	Tyr	Tyr 495	Gly
Tyr Tyr Gly	Tyr Ala 500	Lys A	Ala Arg	Trp 505	Tyr	Cys	Lys	Glu	Cys 510	Ala	Glu
Ser Val Thr 515	Ala Trp	Gly A	Arg Glu 520	Tyr	Ile	Glu	Phe	Val 525	Trp	Lys	Glu
Leu Glu Glu 530	Lys Phe	-	Phe Lys 535	Val	Leu	Tyr	Ile 540	Asp	Thr	Asp	Gly
Leu Tyr Ala 545	Thr Ile	Pro 0	Gly Gly	Glu	Pro	Glu 555	Glu	Ile	Lys	Lys	Lys 560
Ala Leu Glu	Phe Val 565	Lys 1	Tyr Ile	Asn	Ser 570	Lys	Leu	Pro	Gly	Leu 575	Leu
Glu Leu Glu	Tyr Glu 580	Gly F	Phe Tyr	Lys 585	Arg	Gly	Phe	Phe	Val 590	Thr	Lys
Lys Arg Tyr 595	Ala Val	Ile A	Asp Glu 600	Glu	Gly	Lys	Ile	Ile 605	Thr	Arg	Gly
Leu Glu Ile 610	Val Arg		Asp Trp 615	Ser	Glu	Ile	Ala 620	Lys	Glu	Thr	Gln
Ala Lys Val 625	Leu Glu	Ala 1 630	Ile Leu	Lys	His	Gly 635	Asn	Val	Glu	Glu	Ala 640
Val Lys Ile	Val Lys 645	Glu 1	Ile Ile	Glu	Lys 650	Leu	Ala	Lys	Tyr	Glu 655	Ile
Pro Pro Glu	Lys Leu 660	Ala 1	Ile Tyr	Glu 665	Gln	Ile	Thr	Arg	Pro 670	Leu	His
Glu Tyr Lys 675	Ala Ile	Gly E	Pro His 680	Val	Ala	Val	Ala	Lys 685	Lys	Leu	Ala
Ala Arg Gly 690	Val Lys		Lys Pro 695	Gly	Met	Val	Ile 700	Gly	Tyr	Ile	Val
Leu Arg Gly 705	Asp Gly	Pro 1 710	Ile Ser	Lys	Arg	Ala 715	Ile	Leu	Ala	Glu	Glu 720
Phe Asp Pro	Lys Lys 725	His I	Lys Tyr	Asp	Ala 730	Glu	Tyr	Tyr		Glu .735	Asn
Gln Val Leu	Pro Ala 740	Val I	Leu Arg	Ile 745	Leu	Glu	Gly	Phe	Gly 750	Tyr	Arg
		m c	In Lve	Thr	Lvs	Gln	Ala	Glv	Leu	Thr	Δla
Lys Giu Asp 755	Leu Arg	Trp C	760		_,	U 111		765	Dea	1111	1114

Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile 785 790 795 800

Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu

810

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro 820 825 830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn 835 840 845

<210> 31

<211> 845

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid polymerase PhS1 from Figure 11

<400> 31

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile 1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Glu His Asp Arg
20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile 35 40 45

Glu Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile 65 70 75 80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
85 90 95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr 100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

Arg Phe Leu Lys Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr 195 200 205

TYL	Asn 210	Gly	Asp	Ser	Phe	Asp 215	Leu	Pro	Tyr	Leu	Ala 220	Lys	Arg	Ala	Glu
Lys 225	Leu	Gly	Ile	Lys	Leu 230	Thr	Ile	Gly	Arg	Asp 235	Gly	Ser	Glu	Pro	Lys 240
Met	Gln	Arg	Ile	Gly 245	Asp	Met	Thr	Ala	Val 250	Glu	Val	Lys	Gly	Arg 255	Ile
His	Phe	Asp	Leu 260	Tyr	His	Val	Ile	Arg 265	Arg	Thr	Ile	Asn	Leu 270	Pro	Thr
Tyr	Thr	Leu 275	Glu	Ala	Val	Tyr	Glu 280	Ala	Ile	Phe	Gly	Lys 285	Pro	Lys	Glu
Lys	Val 290	Tyr	Ala	Asp	Glu	Ile 295	Ala	Lys	Ala	Trp	Glu 300	Thr	Gly	Glu	Gly
Leu 305	Glu	Arg	Val	Ala	Lys 310	Tyr	Ser	Met	Glu	Asp 315	Ala	Lys	Ala	Thr	Tyr 320
Glu	Leu	Gly	Lys	Glu 325	Phe	Phe	Pro	Met	Glu 330	Ala	Gln	Leu	Ser	Arg 335	Leu
Val	Gly	Gln	Pro 340	Leu	Trp	Asp	Val	Ser 345	Arg	Ser	Ser	Thr	Gly 350	Asn	Leu
Val	Glu	Trp 355	Phe	Leu	Leu	Arg	Lys 360	Ala	Tyr	Glu	Arg	Asn 365	Glu	Leu	Ala
Pro	370	Lys	Pro	Asp	Glu	Arg 375	Glu	Tyr	Glu	Arg	Arg 380	Leu	Arg	Glu	Ser
	370	-		Phe		375					380		Arg		
Tyr 385	370 Ala	Gly	Gly	Phe	Val 390	375 Lys	Glu	Pro	Glu	Lys 395	380 Gly	Leu		Glu	Asn 400
Tyr 385 Ile	370 Ala Val	Gly	Gly Leu	Phe Asp 405	Val 390 Phe	375 Lys Arg	Glu Ala	Pro Leu	Glu Tyr 410	Lys 395 Pro	380 Gly Ser	Leu Ile	Trp	Glu Ile 415	Asn 400 Thr
Tyr 385 Ile His	370 Ala Val Asn	Gly Ser Val	Gly Leu Ser 420	Phe Asp 405	Val 390 Phe Asp	375 Lys Arg Thr	Glu Ala Leu	Pro Leu Asn 425	Glu Tyr 410 Arg	Lys 395 Pro Glu	380 Gly Ser	Leu Ile Cys	Trp Ile Arg	Glu Ile 415 Asn	Asn 400 Thr
Tyr 385 Ile His	370 Ala Val Asn Val	Gly Ser Val Ala 435	Gly Leu Ser 420 Pro	Phe Asp 405 Pro	Val 390 Phe Asp	375 Lys Arg Thr	Glu Ala Leu His 440	Pro Leu Asn 425 Lys	Glu Tyr 410 Arg	Lys 395 Pro Glu Cys	380 Gly Ser Gly Lys	Leu Ile Cys Asp	Trp Ile Arg 430	Glu Ile 415 Asn Pro	Asn 400 Thr Tyr
Tyr 385 Ile His Asp	370 Ala Val Asn Val Ile 450	Gly Ser Val Ala 435 Pro	Gly Leu Ser 420 Pro	Phe Asp 405 Pro Glu Leu	Val 390 Phe Asp Val Leu	375 Lys Arg Thr Gly Lys 455	Glu Ala Leu His 440 Arg	Pro Leu Asn 425 Lys	Glu Tyr 410 Arg Phe	Lys 395 Pro Glu Cys	380 Gly Ser Gly Lys	Leu Ile Cys Asp 445	Trp Ile Arg 430 Phe	Glu Ile 415 Asn Pro	Asn 400 Thr Tyr Gly
Tyr 385 Ile His Asp Phe Lys 465	370 Ala Val Asn Val Ile 450 Thr	Gly Ser Val Ala 435 Pro	Gly Leu Ser 420 Pro Ser	Phe Asp 405 Pro Glu Leu	Val 390 Phe Asp Val Leu Ala 470	Arg Thr Gly Lys 455 Ser	Glu Ala Leu His 440 Arg	Pro Leu Asn 425 Lys Leu Asp	Glu Tyr 410 Arg Phe Leu Pro	Lys 395 Pro Glu Cys Asp Ile 475	380 Gly Ser Gly Lys Glu 460	Leu Ile Cys Asp 445 Arg	Trp Ile Arg 430 Phe Gln	Glu Ile 415 Asn Pro Lys Met	Asn 400 Thr Tyr Gly Ile Leu 480
Tyr 385 Ile His Asp Phe Lys 465 Asp	370 Ala Val Asn Val Ile 450 Thr	Gly Ser Val Ala 435 Pro Lys	Gly Leu Ser 420 Pro Ser Met	Phe Asp 405 Pro Glu Leu Lys Arg 485	Val 390 Phe Asp Val Leu Ala 470	375 Lys Arg Thr Gly Lys 455 Ser	Glu Ala Leu His 440 Arg Gln Lys	Pro Leu Asn 425 Lys Leu Asp	Glu Tyr 410 Arg Phe Leu Pro Leu 490	Lys 395 Pro Glu Cys Asp Ile 475 Ala	380 Gly Ser Gly Lys Glu 460 Glu	Leu Ile Cys Asp 445 Arg Lys	Trp Ile Arg 430 Phe Gln Ile	Glu Ile 415 Asn Pro Lys Met Tyr 495	Asn 400 Thr Tyr Gly Ile Leu 480 Gly

Leu (Glu 530	Glu	Lys	Phe	Gly	Phe 535	Lys	Val	Leu	Tyr	Ile 540	Asp	Thr	Asp	Gly
Leu 1 545	Tyr	Ala	Thr	Ile	Pro 550	Gly	Gly	Lys	Ser	Glu 555	Glu	Ile	Lys	Lys	Lys 560
Ala 1	Leu	Glu	Phe	Val 565	Asp	Tyr	Ile	Asn	Ala 570	Lys	Leu	Pro	Gly	Leu 575	Leu
Glu 1	Leu	Glu	Tyr 580	Glu	Gly	Phe	Tyr	Lys 585	Arg	Gly	Phe	Phe	Val 590	Thr	Lys
Lys 1	Lys	Tyr 595	Ala	Leu	Ile	Asp	Glu 600	Glu	Gly	Lys	Ile	Ile 605	Thr	Arg	Gly
Leu (Glu 610	Ile	Val	Arg	Arg	Asp 615	Trp	Ser	Glu	Ile	Ala 620	Lys	Glu	Thr	Gln
Ala 2 625	Arg	Val	Leu	Glu	Ala 630	Ile	Leu	Lys	His	Gly 635	Asn	Val	Glu	Glu	Ala 640
Val A	Arg	Ile	Val	Lys 645	Glu	Val	Thr	Gln	Lys 650	Leu	Ser	Lys	Tyr	Glu 655	Ile
Pro 1	Pro	Glu	Lys 660	Leu	Ala	Ile	Tyr	Glu 665	Gln	Ile	Thr	Arg	Pro 670	Leu	His
Glu '	Tyr	Lys 675	Ala	Ile	Gly	Pro	His 680	Val	Ala	Val	Ala	Lys 685	Arg	Leu	Ala
Ala	Lys 690	Gly	Val	Lys	Ile	Lys 695	Pro	Gly	Met	Val	Ile 700	Gly	Tyr	Ile	Val
Leu 7	Arg	Gly	Asp	Gly	Pro 710	Ile	Ser	Asn	Arg	Ala 715	Ile	Leu	Ala	Glu	Glu 720
Tyr i	Asp	Pro	Arg	Lys 725	His	Lys	Tyr	Asp	Ala 730	Glu	Tyr	Tyr	Ile	Glu 735	Asn
Gln '	Val	Leu	Pro 740	Ala	Val	Leu	Arg	Ile 745	Leu	Glu	Gly	Phe	Gly 750	Tyr	Arg
Lys (Glu	Asp 755	Leu	Arg	Trp	Gln	Lys 760	Thr	Lys	Gln	Thr	Gly 765	Leu	Thr	Ser
Trp !	Leu 770	Asn	Ile	Lys	Lys	Ser 775	Gly	Thr	Gly	Gly	Gly 780	Gly	Ala	Thr	Val
Lys 1	Phe	Lys	Tyr	Lys	Gly	Glu	Glu	Lys	Glu	Val 795	Asp	Ile	Ser	Lys	Ile 800
, 0 5					790					193					
Lys 1		Val	Trp	Arg 805		Gly	Lys	Met	Ile 810		Phe	Thr	Tyr	Asp 815	
	Lys			805	Val				810	Ser				815	Glu

- <210> 32
- <211> 845
- <212> PRT
- <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid polymerase PhS2 from Figure 11

<400> 32

- Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
 1 5 10 15
- Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg
 20 25 30
- Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
 35 40 45
- Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg 50 55 60
- Ile Ile Asp Ala Glu Lys Val Arg Lys Lys Phe Leu Gly Lys Pro Ile 65 70 75 80
- Glu Val Trp Lys Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95
- Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
- Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125
- Met Glu Gly Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr 130 140
- Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160
- Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 165 170 175
- Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
 180 185 190
- Arg Phe Leu Lys Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr 195 200 205
- Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu 210 215 220
- Lys Leu Gly Ile Lys Leu Pro Ile Gly Arg Asp Gly Ser Glu Pro Lys 225 230 235 240
- Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
 245 250 255
- His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
 260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 280 Lys Val Tyr Ala His Glu Ile Ala Glu Ala Trp Glu Ser Gly Glu Gly 295 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr 310 Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ile Gln Leu Ser Arg Leu 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala Pro Asn Lys Pro Ser Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn 390 395 Ile Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Thr 405 His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Glu Tyr 425 Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Ile Leu Leu Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly 490 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 500 Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Arg Lys Glu 520 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly 530 535 Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys 550 Ala Leu Glu Phe Val Asp Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu 565 570 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys 580 585 590

Lys Arg Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly 600 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln 615 Ala Lys Val Leu Glu Thr Ile Leu Lys His Gly Asn Val Glu Glu Ala 630 635 Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile 650 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Pro Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala Arg Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu 710 715 Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn 725 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg 745 Lys Glu Asp Leu Arg Tyr Gln Lys Thr Lys Gln Val Asp Leu Thr Ala Cys Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn 835 840 845

<210> 33

<211> 145

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid
 polymerase PhS3 from Figure 11

<400> 33

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Ile Ile 1 5 10 15 Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Val Glu Tyr Asp Arg

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile 35 40 45

Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile 65 70 75 80

Glu Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95

Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr 100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Gly Val Arg Tyr Arg Asn Pro Leu Ser Arg Arg Arg Val 130 135 140

Trp 145

<210> 34

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid polymerase PhS4 from Figure 11

<400> 34

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile 1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg 20 25 30

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile 35 40 45

Asp Glu Val Arg Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 60

Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile 65 70 75 80

Glu Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Ala Ile

Arg Glu Lys Val Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr 100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met	Glu 130	Gly	Glu	Glu	Glu	Leu 135	Lys	Leu	Leu	Ala	Phe 140	Asp	Ile	Glu	Thr
Leu 145	Tyr	His	Glu	Gly	Glu 150	Glu	Phe	Ala	Lys	Gly 155	Pro	Ile	Ile	Met	Ile 160
Ser	Tyr	Ala	Asp	Glu 165	Asn	Glu	Ala	Lys	Val 170	Ile	Thr	Trp	Lys	Lys 175	Ile
Asp	Leu	Pro	Tyr 180	Val	Glu	Val	Val	Ser 185	Ser	Glu	Arg	Glu	Met 190	Ile	Lys
Arg	Phe	Leu 195	Arg	Val	Ile	Arg	Glu 200	Lys	Asp	Pro	Asp	Val 205	Ile	Val	Thr
Tyr	Asn 210	Gly	Asp	Ser	Phe	Asp 215	Leu	Pro	Tyr	Leu	Val 220	Lys	Arg	Ala	Glu
Lys 225	Leu	Gly	Ile	Lys	Leu 230	Pro	Ile	Gly	Arg	Asp 235	Gly	Ser	Glu	Pro	Lys 240
Met	Gln	Arg	Ile	Gly 245	Asp	Met	Thr	Ala	Val 250	Glu	Ile	Lys	Gly	Arg 255	Ile
His	Phe	Asp	Leu 260	Tyr	His	Val	Ile	Arg 265	Arg	Thr	Ile	Asn	Leu 270	Pro	Thr
Tyr	Thr	Leu 275	Glu	Ala	Val	Tyr	Glu 280	Ala	Ile	Phe	Gly	Lys 285	Pro	Lys	Glu
Lys	Val 290	Tyr	Ala	His	Glu	Ile 295	Ala	Lys	Ala	Trp	Glu 300	Ser	Gly	Glu	Gly
Leu 305	Glu	Arg	Val	Ala	Lys 310	Tyr	Ser	Met	Glu	Asp 315	Ala	Lys	Val	Thr	Tyr 320
Glu	Leu	Gly	Lys	Glu 325	Phe	Leu	Pro	Met	Glu 330	Ile	Gln	Leu	Ser	Arg 335	Leu
Val	Gly	Gln	Pro 340	Leu	Trp	Asp	Val	Ser 345	Arg	Ser	Ser	Thr	Gly 350	Asn	Leu
Val	Glu	Trp 355	Phe	Leu	Leu	Arg	Lys 360	Ala	Tyr	Glu	Arg	Asn 365	Glu	Val	Ala
Pro	Asn 370	Lys	Pro	Ser	Glu	Glu 375	Glu	Tyr	Glu	Arg	Arg 380	Leu	Arg	Glu	Ser
Tyr 385	Ala	Gly	Gly	Tyr	Val 390	Lys	Glu	Pro	Glu	Lys 395	Gly	Leu	Trp	Glu	Asn 400
Ile	Val	Ser	Leu	Asp 405	Phe	Arg	Ser	Leu	Tyr 410	Pro	Ser	Ile	Ile	Ile 415	Thr
His	Asn	Val	Ser 420	Pro	Asp	Thr	Leu	Asn 425	Arg	Glu	Gly	Cys	Lys 430	Asn	Tyr
Asp	Ile	Ala 435	Pro	Gln	Val	Gly	His 440	Lys	Phe	Cys	Lys	Asp 445	Ile	Pro	Gly

Phe	Ile 450	Pro	Ser	Leu	Leu	Lys 455	His	Leu	Leu	Asp	Glu 460	Arg	Gln	Lys	Ile
Lys 465	Arg	Lys	Met	Lys	Glu 470	Ser	Gln	Asp	Pro	Ile 475	Glu	Lys	Lys	Met	Leu 480
Asp	Tyr	Arg	Gln	Arg 485	Ala	Ile	Lys	Leu	Leu 490	Ala	Asn	Ser	Tyr	Tyr 495	Gly
Tyr	Tyr	Gly	Tyr 500	Ala	Lys	Ala	Arg	Trp 505	Tyr	Cys	Lys	Glu	Cys 510	Ala	Glu
Ser	Val	Thr 515	Ala	Trp	Gly	Arg	Glu 520	Tyr	Ile	Glu	Phe	Val 525	Arg	Lys	Glu
Leu	Glu 530	Glu	Lys	Phe	Gly	Phe 535	Lys	Val	Leu	Tyr	Ile 540	Asp	Thr	Gly	Leu
Tyr 545	Ala	Thr	Ile	Pro	Gly 550	Ala	Lys	Ser	Glu	Glu 555	Ile	Lys	Lys	Lys	Ala 560
Leu	Glu	Phe	Val	Lys 565	Tyr	Ile	Asn	Ser	Lys 570	Leu	Pro	Gly	Leu	Leu 575	Glu
Leu	Glu	Tyr	Glu 580	Gly	Phe	Tyr	Val	Arg 585	Gly	Phe	Phe	Val	Thr 590	Lys	Lys
Arg	Tyr	Ala 595	Leu	Ile	Asp	Glu	Glu 600	Gly	Lys	Ile	Ile	Thr 605	Arg	Gly	Leu
Glu	Ile 610	Val	Arg	Arg	Asp	Trp 615	Ser	Glu	Ile	Ala	Lys 620	Glu	Thr	Gln	Ala
Arg 625	Val	Leu	Glu	Thr	Ile 630	Leu	Lys	His	Gly	Asn 635	Val	Glu	Glu	Ala	Val 640
Arg	Ile	Val	Lys	Glu 645	Val	Thr	Lys	Lys	Leu 650	Ser	Asn	Tyr	Glu	Ile 655	Pro
Pro	Glu	Lys	Leu 660	Ala	Ile	Tyr	Glu	Gln 665	Ile	Thr	Arg	Pro	Leu 670	His	Glu
Tyr	Lys	Ala 675	Ile	Gly	Pro	His	Val 680	Ala	Val	Ala	Lys	Arg 685	Leu	Ala	Ala
Lys	Gly 690	Val	Lys	Ile	Arg	Pro 695	_	Met	Val	Ile	Gly 700	Tyr	Ile	Val	Leu
Arg 705	Gly	Asp	Gly	Pro	Ile 710	Ser	Asn	Arg	Ala	Ile 715	Leu	Ala	Glu	Glu	Tyr 720
Asp	Pro	Lys	Lys	His 725	Lys	Tyr	Asp		Glu 730	Tyr	Tyr	Ile	Glu	Asn 735	Gln
Val	Leu	Pro	Ala 740	Val	Leu	Arg	Ile	Leu 745	Glu	Ala	Phe	Gly	Tyr 750	Arg	Lys
Glu	Asp	Leu 755	Arg	Trp	Gln	Lys	Thr 760	Lys	Gln	Val	Gly	Leu 765	Thr	Ala	Trp

- Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val Lys
 770 780
- Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys 785 790 795 . 800
- Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly 805 810 815
- Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys 820 825 830
- Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn 835 840
- <210> 35
- <211> 845
- <212> PRT
- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence:hybrid
 polymerase PhS5 from Figure 11
- <400> 35
- Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile 1 5 10 15
- Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg 20 25 30
- Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile 35 40 45
- Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
 50 55 60
- Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile 65 70 75 80
- Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile 85 90 95
- Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr 100 105 110
- Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125
- Met Glu Gly Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 130 135 140
- Leu Tyr His Glu Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160
- Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 165 170 175
- Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr 200 Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu 215 Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys 230 235 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile 250 His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 280 Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr 310 315 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu 325 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu 345 Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn 385 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ihr 410 His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr 425 Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe Ile Pro Ser Leu Leu Lys His Leu Leu Asp Glu Arg Gln Glu Ile 450 455 Lys Arg Lys Met Lys Ala Ser Lys Asp Pro Ile Glu Lys Lys Met Leu Asp Tyr Arg Gln Arg Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly 490 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu 500 505 510

Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Leu Val Trp Lys Glu 520 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly 535 Leu Tyr Ala Thr Ile Pro Gly Gly Lys Pro Glu Glu Ile Lys Lys 555 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu 570 Glu Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala 635 630 Val Lys Ile Val Lys Glu Val Thr Gln Lys Leu Ala Lys Tyr Glu Ile 650 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg 745 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser 760 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val 775 780 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu 805 810 815

Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro 820 825 830

Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Asn 835 840 845

<210> 36

<211> 472

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hybrid polymerase PhS6 from Figure 11

<400> 36

Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile 1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile 35 40 45

Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg
50 60

Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80

Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile 85 90 95

Arg Asp Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125

Met Glu Gly Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr 130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 180 185 190

Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr 195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu 210 215 220

Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys 225 230 235 240 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile 250 245 His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr 265 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 280 Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Tyr Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala 360 Pro Asn Lys Pro Asp Glu Glu Glu Tyr Glu Arg Arg Leu Arg Glu Ser Tyr Thr Gly Gly Tyr Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn 390 395 Leu Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu Tyr Asp Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly 435 Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Glu Glu Arg Gln Lys Ile 460 455 Lys Arg Lys Met Lys Ala Thr Asn 465 470 <210> 37 <211> 844 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence:hybrid polymerase Sso7d fusion protein PhS7 <400> 37. Met Ile Leu Asp Ala Asp Tyr Ile Thr Glu Asp Gly Lys Pro Ile Ile

10

30

Arg Leu Phe Lys Lys Glu Asn Gly Glu Phe Lys Val Glu Tyr Asp Arg

25

5

20

Asn Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Gln Ile 40 Asp Glu Val Lys Lys Ile Thr Ala Glu Arg His Gly Lys Ile Val Arg Ile Ile Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Ala Ile Arq Asp Lys Val Arq Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr 105 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro Met Glu Gly Glu Glu Leu Lys Leu Leu Ala Phe Asp Ile Glu Thr Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 150 Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Lys Ile Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys 1.85 Arg Phe Leu Arg Val Ile Arg Glu Lys Asp Pro Asp Ile Ile Ihr Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu Lys Leu Gly Ile Lys Leu Pro Leu Gly Arg Asp Gly Ser Glu Pro Lys Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Ile Lys Gly Arg Ile His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr 260 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu Lys Val Tyr Ala Asp Glu Ile Ala Glu Ala Trp Glu Ser Gly Lys Asn 290 295 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr 310 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu 325 330 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu 340 345 350

Val Gl	u Trp 355	Tyr	Leu	Leu	Arg	Lys 360	Ala	Tyr	Glu	Arg	Asn 365	Glu	Val	Ala
Pro As		Pro	Asp	Glu	Glu 375	Glu	Tyr	Glu	Arg	Arg 380	Leu	Arg	Glu	Ser
Tyr Th	r Gly	Gly	Tyr	Val 390	Lys	Glu	Pro	Glu	Lys 395	Gly	Leu	Trp	Glu	Asn 400
Leu Va	l Ser	Leu	Asp 405	Phe	Arg	Ala	Leu	Tyr 410	Pro	Ser	Ile	Ile	Ile 415	Thr
His As	n Val	Ser 420	Pro	Asp	Thr	Leu	Asn 425	Arg	Glu	Gly	Cys	Arg 430	Asn	Tyr
Asp Va	l Ala 435	Pro	Gln	Val	Gly	His 440	Lys	Phe	Cys	Lys	Asp 445	Phe	Pro	Gly
Phe Il 45		Ser	Leu	Leu	Gly 455	Arg	Leu	Leu	Glu	Glu 460	Arg	Gln	Glu	Ile
Lys Th	r Lys	Met	Lys	Ala 470	Thr	Lys	Asp	Pro	Ile 475	Glu	Lys	Lys	Leu	Leu 480
Asp Ty	r Arg	Gln	Lys 485	Ala	Ile	Lys	Ile	Leu 490	Ala	Asn	Ser	Phe	Tyr 495	Gly
Tyr Ty	r Gly	Tyr 500	Ala	Lys	Ala	Arg	Trp 505	Tyr	Cys	Lys	Glu	Cys 510	Ala	Glu
Ser Va	l Thr 515	Ala	Trp	Gly	Arg	Lys 520	Tyr	Ile	Glu	Phe	Val 525	Arg	Lys	Glu
Leu Gl 53		Lys	Phe	Gly	Phe 535	Lys	Val	Leu	Tyr	Ile 540	Asp	Thr	Asp	Gly
Leu Ty 545	r Ala	Thr	Ile	Pro 550	Gly	Gly	Lys	Pro	Glu 555	Glu	Ile	Lys	ГÀż	Lys 560
Ala Le	u Glu	Phe	Val 565	Lys	Tyr	Ile	Asn	Ser 570	Lys	Leu	Pro	Gly	Leu 575	Leu
Glu Le	u Glu	Tyr 580	Glu	Gly	Phe	Tyr	Val 585	Arg	Gly	Phe	Phe	Val 590	Thr	Lys
Lys Ar	g Tyr 595	Ala	Val	Ile	Asp	Glu 600	Glu	Gly	Lys	Ile	Ile 605	Thr	Arg	Gly
Leu Gl 61		Val	Arg	Arg	Asp 615	Trp	Ser	Glu	Ile	Ala 620	Lys	Glu	Thr	Gln
Ala Ar 625	g Val	Leu	Glu	Ala 630	Ile	Leu	Lys	His	Gly 635	Asn	Val	Glu	Glu	Ala 640
Val Ly	s Ile	Val	Lys 645	Glu	Val	Thr	Gln	Lys 650	Leu	Ala	Lys	Tyr	Glu 655	Ile

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Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
                              680
 Ala Arg Gly Val Lys Val Arg Pro Gly Met Val Ile Gly Tyr Ile Val
                         695
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
                                          715
                     710
 Tyr Asp Leu Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
                                     730
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Ala Phe Gly Tyr Arg
                                  745
 Lys Glu Asp Leu Arg Trp Gln Lys Thr Lys Gln Val Gly Leu Thr Ser
 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
                                          795
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
                  805
 Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
                                 825
 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
 <210> 38
 <211> 6
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. <220>
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       polyhistidine epitope tag, metal chelate affinity
       ligand
 <400> 38
 His His His His His
  1
 <210> 39
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       epitope tag
  Asp Tyr Lys Asp Asp Asp Lys
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1

5

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<210> 40
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
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      primer oligonucleotide
ttggtaccaa gcttcatatg a
                                                                    21
<210> 41
<211> 51
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Fwd 2 PCR
      primer oligonucleotide
<400> 41
ccgctgccga sctatgcgac cyctcacagc kcaggcctgg atctgcgtgc g
                                                                    51
<210> 42
<211> 69
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Fwd 3 PCR
      primer oligonucleotide
<400> 42
ttccgaccgg tctgatcmtt sawattscgg awggttmtgm ggsgcagrtg ckgccgcgta 60
                                                                    69
gcggcctgg
<210> 43
<211> 98
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Fwd 4 PCR
      primer oligonucleotide
<400> 43
ttttgatcga trscgattat crgggcsaas tgawgrttak cstggtgaac ckgggcmasg 60
                                                                    98
awgaakttry gattsagcsg ggcgaacgta ttgcgcag
<210> 44
<211> 56
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Fwd 5 PCR
      primer oligonucleotide
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cgtggcgaag gcggctttgg ctctascggc asamagtaat gaggatccga attctt
                                                                    56
<210> 45
<211> 89
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Rev A PCR
      primer oligonucleotide
<400> 45
ggtcgcatag stcggcagcg gwaawtcttk gscatgasgc rgacgcwkaa ttttcasawy 60
aaytttkytc atatgaagct tggtaccaa
<210> 46
<211> 83
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Rev B PCR
      primer oligonucleotide
<400> 46
gatcagaccg gtcggaayca gcrycstwtc ammcggckya akttycascg swtystyaak 60
                                                                    83
gsmcgcacgc agatccaggc ctg
<210> 47
<211> 68
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Rev C PCR
      primer oligonucleotide
<400> 47
ttttatcgat crkgcccrsc gcgttcagca scrytawgcc mtktttccag sccaggccgc 60
tacgcggc
<210> 48
<211> 107
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Rev D PCR
      primer oligonucleotide
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<400> 48
tagagccaaa gccgccttcg ccacgmtsgg tctgagaaam wtcttccacc wsawyaamtt 60
ccrccygcws caccggcrca awaaycakct gcgcaatacg ttcgccc
<210> 49
<211> 22
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Rev D PCR
      primer oligonucleotide
<400> 49
aagaattcgg atcctcatta ct
                                                                    22
<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence:primer to
      measure exonuclease activity
<220>
<221> modified base
<222> (1)
<223> n = t modified by 6-carboxy-fluorescein (FAM)
<221> modified base
<222> (45)
<223> n = t amino-linked to quencher
      4-(4-dimethylaminophenylazo)benzoyl group (dabcyl,
      DAB)
<400> 50
ntttttgagg tgtgtcctac acagcggagt gtaggacaca cctcn
                                                                   45
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